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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=8; day=29; hr=11; min=59; sec=49; ms=434;]

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Application No: 10591852

Version No: 1.0

Input Set:

Output Set:

Started: 2008-07-24 18:50:29.358

Finished: 2008-07-24 18:50:32.402

Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 44 ms

Total Warnings: 146

Total Errors: 0

No. of SeqIDs Defined: 205

Actual SeqID Count: 205

Error code	Error Description
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Error code

Error Description

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SEQUENCE LISTING

<110> Weyler, Walter
Hsu, Amy Kuang-Hua

<120> pckA Modifications and Enhanced Protein Expression in Bacillus

<130> GC836-US

<140> 10591852

<141> 2008-07-24

<150> PCT/US2005/011821

<151> 2005-04-07

<150> US 60/561,110

<151> 2004-04-09

<160> 205

<170> PatentIn version 3.2

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<211> 129

<212> DNA

<213> Bacillus subtilis

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<211> 43

<212> PRT

<213> Bacillus subtilis

<400> 2

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Ala Gly Ala Thr Gly Leu Phe Gly Leu Trp Gly	
35 40	

<210> 3

<211> 456

<212> DNA

<213> Bacillus subtilis

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aatccgtccg ttcaattttt aaaaaaagtt tctgccacac tggaagttga attaacagaa	180
ttatttgacg cagaaacaat gatgtatgaa aaaatcagcg gcggtgaaga agaatggcgc	240
gtacatttag tgcaagccgt acaagccggg atggaaaagg aagaattggt cacttttacg	300

aacagactca	agaaagaaca	gcctgaaact	gcctcttacc	gcaaccgcaa	actgacggaa	360
tccaatatag	aagaatggaa	agcgctgatg	gcggaggcaa	gagaaatcgg	cttgtctgtc	420
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 <212> PRT
 <213> Bacillus subtilis

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 20 25 30
 Lys Ile Glu Arg Gly Val His Thr Asn Pro Ser Val Gln Phe Leu Lys
 35 40 45
 Lys Val Ser Ala Thr Leu Glu Val Glu Leu Thr Glu Leu Phe Asp Ala
 50 55 60
 Glu Thr Met Met Tyr Glu Lys Ile Ser Gly Gly Glu Glu Glu Trp Arg
 65 70 75 80
 Val His Leu Val Gln Ala Val Gln Ala Gly Met Glu Lys Glu Glu Leu
 85 90 95
 Phe Thr Phe Thr Asn Arg Leu Lys Lys Glu Gln Pro Glu Thr Ala Ser
 100 105 110
 Tyr Arg Asn Arg Lys Leu Thr Glu Ser Asn Ile Glu Glu Trp Lys Ala
 115 120 125
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 130 135 140
 Ser Phe Leu Lys Thr Lys Gly Arg
 145 150

<210> 5
 <211> 165
 <212> DNA
 <213> Bacillus subtilis

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 <211> 55
 <212> PRT
 <213> Bacillus subtilis

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 1 5 10 15
 Met Lys Pro Gly Gly Thr Ser Ile Val Lys Ala Ala Gly Cys Met Gly
 20 25 30
 Cys Trp Ala Ser Lys Ser Ile Ala Met Thr Arg Val Cys Ala Leu Pro
 35 40 45
 His Pro Ala Met Arg Ala Ile
 50 55

<210> 7

<211> 831
<212> DNA
<213> Bacillus subtilis

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gatcaaaaagc gccggggcga acagctgaca agtatctttg aaaacggcac aacgggagatc 180
caatatggat atgtagagcg attggatgac gggcgaggct atacatgcgg acgggcaggc 240
tttacaacgg ctaccgggga tgcattggaa gtagtggaaag tatacacaaa ggcagttccg 300
aataacaaaac tgaaaaagta tctgcctgaa ttgcgcgcgc tggccaagga agaaagcgat 360
gatacaagca atctcaaggg attcgttctt gcctggaagt cgcttgcaaa tgataaggaa 420
tttcgcgcgc ctcaagacaa agtaaattgac catttgattt atcagcctgc catgaaacga 480
tcggataatg cgggactaaa aacagcattg gcaagagctg tgatgtacga tacggttatt 540
cagcatggcg atggtgatga ccctgactct ttttatgcct tgattaaacg tacgaacaaa 600
aaagcggggcg gatcacctaa agacggaata gacgagaaga agtggttgaa taaattcttg 660
gacgtacgct atgacgatct gatgaatccg gccaatcatg acaccctga cgaatggaga 720
gaatcagttg cccgtgtgga cgtgcttcgc tctatcgcca aggagaacaa ctataatcta 780
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<210> 8
<211> 277
<212> PRT
<213> Bacillus subtilis

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Val Phe Ala Ala Gly Leu Asn Lys Asp Gln Lys Arg Arg Ala Glu Gln
35 40 45
Leu Thr Ser Ile Phe Glu Asn Gly Thr Thr Glu Ile Gln Tyr Gly Tyr
50 55 60
Val Glu Arg Leu Asp Asp Gly Arg Gly Tyr Thr Cys Gly Arg Ala Gly
65 70 75 80
Phe Thr Thr Ala Thr Gly Asp Ala Leu Glu Val Val Glu Val Tyr Thr
85 90 95
Lys Ala Val Pro Asn Asn Lys Leu Lys Lys Tyr Leu Pro Glu Leu Arg
100 105 110
Arg Leu Ala Lys Glu Glu Ser Asp Asp Thr Ser Asn Leu Lys Gly Phe
115 120 125
Ala Ser Ala Trp Lys Ser Leu Ala Asn Asp Lys Glu Phe Arg Ala Ala
130 135 140
Gln Asp Lys Val Asn Asp His Leu Tyr Tyr Gln Pro Ala Met Lys Arg
145 150 155 160
Ser Asp Asn Ala Gly Leu Lys Thr Ala Leu Ala Arg Ala Val Met Tyr
165 170 175
Asp Thr Val Ile Gln His Gly Asp Gly Asp Asp Pro Asp Ser Phe Tyr
180 185 190
Ala Leu Ile Lys Arg Thr Asn Lys Lys Ala Gly Gly Ser Pro Lys Asp
195 200 205
Gly Ile Asp Glu Lys Lys Trp Leu Asn Lys Phe Leu Asp Val Arg Tyr
210 215 220
Asp Asp Leu Met Asn Pro Ala Asn His Asp Thr Arg Asp Glu Trp Arg
225 230 235 240
Glu Ser Val Ala Arg Val Asp Val Leu Arg Ser Ile Ala Lys Glu Asn

	245		250		255										
Asn	Tyr	Asn	Leu	Asn	Gly	Pro	Ile	His	Val	Arg	Ser	Asn	Glu	Tyr	Gly
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	275														

<210> 9
 <211> 792
 <212> DNA
 <213> Bacillus subtilis

<400> 9

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acaaatctgg	ttgacatgct	tgcgaaaaaa	tactcaaaag	gcaaaagctt	ccacgaggat	180
ctccgccagg	tcggcatgat	cgggctgcta	ggcgcgatta	agcgatacga	tcctgttgtc	240
ggcaaatcgt	ttgaagcttt	tgcaatcccg	acaatcatcg	gtgaaattaa	acgtttcctc	300
agagataaaa	catggagcgt	tcatgtgccg	agacgaatta	aagaactcgg	tccaagaatc	360
aaaatggcgg	ttgatcagct	gaccactgaa	acacaaagat	cgccgaaagt	cgaagagatt	420
gccgaattcc	tcgatgtttc	tgaagaagag	gttcttgaaa	cgatggaaat	gggcaaaagc	480
tatcaagcct	tatccgttga	ccacagcatt	gaagcggatt	cggacggaag	cactgtcacg	540
attcttgata	tcgtcggatc	acaggaggac	ggatatgagc	gggtcaacca	gcaattgatg	600
ctgcaaagcg	tgtttcatgt	cctttcagac	cgtgagaaac	aaatcataga	ccttacgtat	660
attcaaaaca	aaagccaaaa	agaaactggg	gacattctcg	gtatatctca	aatgcacgtc	720
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<210> 10
 <211> 264
 <212> PRT
 <213> Bacillus subtilis

<400> 10

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			20					25					30		
Gln	Glu	Thr	Leu	Val	Arg	Val	Tyr	Thr	Asn	Leu	Val	Asp	Met	Leu	Ala
			35					40					45		
Lys	Lys	Tyr	Ser	Lys	Gly	Lys	Ser	Phe	His	Glu	Asp	Leu	Arg	Gln	Val
			50				55				60				
Gly	Met	Ile	Gly	Leu	Leu	Gly	Ala	Ile	Lys	Arg	Tyr	Asp	Pro	Val	Val
							70			75				80	
Gly	Lys	Ser	Phe	Glu	Ala	Phe	Ala	Ile	Pro	Thr	Ile	Ile	Gly	Glu	Ile
							85			90				95	
Lys	Arg	Phe	Leu	Arg	Asp	Lys	Thr	Trp	Ser	Val	His	Val	Pro	Arg	Arg
			100					105					110		
Ile	Lys	Glu	Leu	Gly	Pro	Arg	Ile	Lys	Met	Ala	Val	Asp	Gln	Leu	Thr
			115					120					125		
Thr	Glu	Thr	Gln	Arg	Ser	Pro	Lys	Val	Glu	Glu	Ile	Ala	Glu	Phe	Leu
							130					140			
Asp	Val	Ser	Glu	Glu	Glu	Val	Leu	Glu	Thr	Met	Glu	Met	Gly	Lys	Ser
							145					155			160
Tyr	Gln	Ala	Leu	Ser	Val	Asp	His	Ser	Ile	Glu	Ala	Asp	Ser	Asp	Gly
							165			170				175	
Ser	Thr	Val	Thr	Ile	Leu	Asp	Ile	Val	Gly	Ser	Gln	Glu	Asp	Gly	Tyr
							180				185			190	

Glu Arg Val Asn Gln Gln Leu Met Leu Gln Ser Val Leu His Val Leu
 195 200 205
 Ser Asp Arg Glu Lys Gln Ile Ile Asp Leu Thr Tyr Ile Gln Asn Lys
 210 215 220
 Ser Gln Lys Glu Thr Gly Asp Ile Leu Gly Ile Ser Gln Met His Val
 225 230 235 240
 Ser Arg Leu Gln Arg Lys Ala Val Lys Lys Leu Arg Glu Ala Leu Ile
 245 250 255
 Glu Asp Pro Ser Met Glu Leu Met
 260

<210> 11
 <211> 744
 <212> DNA
 <213> *Bacillus subtilis*

<400> 11
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 tgggtatttgc tgtttgttct gggcgctatg gtatactgga catatgagcc cacttcctta 180
 tttaccact gggaacggta tctcattgtc gcagtcagtt ttgctttgat tgatgctttt 240
 atcttcttaa gtgcatatgt caaaaaactg gccggcagcg agcttgaaac agacacaaga 300
 gaaattcttg aagaaaacaa cgaaatgctc cacatgtatc tcaatcggtc gaaaacatac 360
 caatacctat tgaaaaacga accgatccat gtttattatg gaagtataga tgcttatgct 420
 gaaggtattg ataagctgct gaaaacctat gctgataaaa tgaacttaac ggcttctctt 480
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 gatgtacaaa cacggctcga tcgaaaggat gtttattacg accaatacgg aaaagtgggt 600
 ctcacccctt ttaccatcga gacacagaac tatgtcatca agctgacgtc tgacagcatt 660
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<210> 12
 <211> 248
 <212> PRT
 <213> *Bacillus subtilis*

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 20 25 30
 Lys Met Ser Ala Ile Arg Lys Thr Trp Tyr Leu Leu Phe Val Leu Gly
 35 40 45
 Ala Met Val Tyr Trp Thr Tyr Glu Pro Thr Ser Leu Phe Thr His Trp
 50 55 60
 Glu Arg Tyr Leu Ile Val Ala Val Ser Phe Ala Leu Ile Asp Ala Phe
 65 70 75 80
 Ile Phe Leu Ser Ala Tyr Val Lys Lys Leu Ala Gly Ser Glu Leu Glu
 85 90 95
 Thr Asp Thr Arg Glu Ile Leu Glu Glu Asn Asn Glu Met Leu His Met
 100 105 110
 Tyr Leu Asn Arg Leu Lys Thr Tyr Gln Tyr Leu Leu Lys Asn Glu Pro
 115 120 125
 Ile His Val Tyr Tyr Gly Ser Ile Asp Ala Tyr Ala Glu Gly Ile Asp
 130 135 140
 Lys Leu Leu Lys Thr Tyr Ala Asp Lys Met Asn Leu Thr Ala Ser Leu
 145 150 155 160

Cys His Tyr Ser Thr Gln Ala Asp Lys Asp Arg Leu Thr Glu His Met
 165 170 175
 Asp Asp Pro Ala Asp Val Gln Thr Arg Leu Asp Arg Lys Asp Val Tyr
 180 185 190
 Tyr Asp Gln Tyr Gly Lys Val Val Leu Ile Pro Phe Thr Ile Glu Thr
 195 200 205
 Gln Asn Tyr Val Ile Lys Leu Thr Ser Asp Ser Ile Val Thr Glu Phe
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 Pro Ile Glu Glu Glu Gly Glu Gly
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<210> 13
 <211> 120
 <212> DNA
 <213> *Bacillus subtilis*

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<210> 14
 <211> 40
 <212> PRT
 <213> *Bacillus subtilis*

<400> 14
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 20 25 30
 His Val Thr Glu Arg Gly Met Thr
 35 40

<210> 15
 <211> 1134
 <212> DNA
 <213> *Bacillus subtilis*

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 gaaattgagg atatggaaga agaccaagat ttgctgctgt attattcttt aatggagtgc 180
 aggcaccgtg tcatgctgga ttacattaag ccttttgagg aggacacgtc gcagctagag 240
 ttttcagaat tgtagaaga catcgaaggg aatcagtaca agctgacagg gcttctcgaa 300
 tattacttta atttttttcg aggaatgtat gaatttaagc agaagatgtt tgtcagtgcc 360
 atgatgtatt ataaacgggc agaaaagaat cttgccctcg tctcggatga tattgagaaa 420
 gcagagtttg cttttaaaat ggctgagatt ttttacaatt taaaacaaac ctatgtttcg 480
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 gagctttttc aattttttaca tgcgttatatc ggaaaaaaca ttgacacaga atcagtctca 960

